amino acid sequence

$$X\text{-}(Cys^{41}\text{-}Cys^{133})\text{-}Y$$

wherein

$(Cys^{41}\text{-}Cys^{133})$ consists of Cys^{41} through Cys^{133} of SEQ ID NO:2;

Y represents the carboxy terminal group of Cys^{133}, a carboxy-terminus amino acid residue of Ile^{134}, or a substituted amino acid residue, and

X represents a methionylated or nonmethionylated amine group of Cys^{41} or amino-terminus amino acid residue(s) selected from the group:

B1 cont

A2 cont

G
RG
NRG
KNRG (SEQ ID NO:3)
GKNRG (SEQ ID NO:4)
RGKNRG (SEQ ID NO:5)
QRGKNRG (SEQ ID NO:6)
GQRGKNRG (SEQ ID NO:7)
RGQRGKNRG (SEQ ID NO:8)
RRGQRGKNRG (SEQ ID NO:9)
G RRGQRGKNRG (SEQ ID NO:10)
KG RRGQRGKNRG (SEQ ID NO:11)
GKG RRGQRGKNRG (SEQ ID NO:12)
RGKG RRGQRGKNRG (SEQ ID NO:13)
SRGKG RRGQRGKNRG (SEQ ID NO:14)
NSRGKG RRGQRGKNRG (SEQ ID NO:15)
ENSRGKG RRGQRGKNRG (SEQ ID NO:16)
PENSRGKG RRGQRGKNRG (SEQ ID NO:17)
NPENSRGKG RRGQRGKNRG (SEQ ID NO:18)
ANPENSRGKG RRGQRGKNRG (SEQ ID NO:19)
A ANPENSRGKG RRGQRGKNRG (SEQ ID NO:20)
AA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:21)
AAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:22)
QAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:23)
RQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:24)
NRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:25)

RNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:26)

ERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:27)

RERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:28)

RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:29)

P RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:30)

LP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:31)

VLP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:32)

AVLP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:33)

MAVLP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:34)

QMAVLP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:35)

KQMAVLP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:36)

DKQMAVLP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:37) and

PDKQMAVLP RRERNRQAAA ANPENSRGKG RRGQRGKNRG (SEQ ID NO:38)

or a substitution or deletion variant of X, wherein said variant is in excess of 70% identical to an amino acid sequence of X as set forth above when four gaps in a length of 100 amino acids may be introduced to assist in that alignment, to provide *in vivo* production of said truncated GDNF protein.

32. (**Amended**) A method according to claim 31 [of treating Parkinson's Disease] comprising implanting in a patient a cell transformed with said [a] polynucleotide [sequence of Claim 13] to provide *in vivo* production of said truncated GDNF protein.

Please add the followng new claims:

-- 45. A method according to Claim 31 or 32, wherein X is selected from the group consisting of SEQ ID NO: 3, 7, 8, 14, 17 and 18.

46. A method according to Claim 31 or 32, wherein X is G, RG or NRG.

47. A method according to Claim 31 or 32, wherein said GDNF protein product has the amino acid sequence of SEQ ID NO:42.

48. A method according to Claim 31 or 32, wherein said GDNF protein product has the amino acid sequence of SEQ ID NO:44.

49. A method according to Claim 31 or 32, wherein said GDNF protein product has the amino acid sequence of SEQ ID NO:46. --

Respectfully submitted,

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